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RAW SEQUENCE LISTING   DATE: 04/04/2002
PATENT APPLICATION: US/09/749,728B   TIME: 14:00:07

Input Set : A:\766.43 Sequence Listing.txt
Output Set: N:\CRF3\04042002\I749728B.raw

```
   3 <110> APPLICANT: Umezawa, Akihiro
   4        Hata, Jun-Ichi
   5        Fukuda, Keiichi
   6        Ogawa, Satoshi
   7        Sakurada, Kazuhiro
   8        Gojo, Satoshi
   9        Yamada, Yoji
  11 <120> TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO
CARDIOMYOCYTES
  13 <130> FILE REFERENCE: 00766.000043
  15 <140> CURRENT APPLICATION NUMBER: US/09/749,728B
  16 <141> CURRENT FILING DATE: 2001-09-17
  18 <150> PRIOR APPLICATION NUMBER: H11-372826
  19 <151> PRIOR FILING DATE: 1999-12-28
  21 <150> PRIOR APPLICATION NUMBER: PCT-JP00-01148
  22 <151> PRIOR FILING DATE: 2000-02-28
  24 <150> PRIOR APPLICATION NUMBER: PCT-JP00-07741
  25 <151> PRIOR FILING DATE: 2000-11-02
  27 <160> NUMBER OF SEQ ID NOS: 80
  29 <170> SOFTWARE: PatentIn Ver.2.0
  31 <210> SEQ ID NO: 1
  32 <211> LENGTH: 411
  33 <212> TYPE: PRT
  34 <213> ORGANISM: Homo sapiens
W--> 35 <400> SEQUENCE: 1
  36 Met Arg Ala His Pro Gly Gly Gly Arg Cys Cys Pro Glu Gln Glu Glu
  37  1               5                  10                  15
  38 Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile
  39             20                  25                  30
  40 Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly
  41             35                  40                  45
  42 Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
  43       50                  55                  60
  44 Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
  45  65                  70                  75                  80
  46 Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
  47             85                  90                  95
  48 Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly
  49             100                 105                 110
  50 Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro
  51             115                 120                 125
  52 Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr
  53       130                 135                 140
  54 Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys
```

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55 145                      150                     155                     160
56 Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp
57                    165                     170                     175
58 Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
59               180                     185                     190
60 Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe
61               195                     200                     205
62 Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg
63      210                     215                     220
64 Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn
65 225                     230                     235                     240
66 Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
67                    245                     250                     255
68 Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
69               260                     265                     270
70 Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln
71               275                     280                     285
72 Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu
73      290                     295                     300
74 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr
75 305                     310                     315                     320
76 Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile
77               325                     330                     335
78 Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu
79               340                     345                     350
80 Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp
81      355                     360                     365
82 Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu
83      370                     375                     380
84 Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu
85 385                     390                     395                     400
86 Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala
87               405                     410
88 <210> SEQ ID NO: 2
89 <211> LENGTH: 1233
90 <212> TYPE: DNA
91 <213> ORGANISM: Homo sapiens
92 <220> FEATURE:
93 <221> NAME/KEY: CDS
94 <223> OTHER INFORMATION: (1)..(1236)
95 <400> SEQUENCE: 2
96 atg cgc gcg cac ccg ggg gga ggc cgc tgc tgc ccg gag cag gag gag    48
97 Met Arg Ala His Pro Gly Gly Gly Arg Cys Cys Pro Glu Gln Glu Glu
98  1               5                       10                      15
99 ggg gag agt gcg gcg ggc ggc agc ggc gct ggc ggc gac tcc gcc ata   96
100 Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile
101               20                      25                      30
102 gag cag ggg ggc cag ggc agc gcg ctc gcc ccg tcc ccg gtg agc ggc   144
103 Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly
```

W--> 92
W--> 95

```
104        35                  40                  45
105 gtg cgc agg gaa ggc gct cgg ggc ggc ggc cgt ggc cgg ggg cgg tgg    192
106 Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
107     50                  55                  60
108 aag cag gcg ggc cgg ggc ggc ggc gtc tgt ggc cgt ggc cgg ggc cgg    240
109 Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
110 65                  70                  75                  80
111 ggc cgt ggc cgg gga cgg gga cgg ggc cgg ggc cgg ggc cgc ggc cgt    288
112 Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
113             85                  90                  95
114 ccc ccg agt ggc ggc agc ggc ctt ggc ggc gac ggc ggc ggc tgc ggc    336
115 Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly
116             100                 105                 110
117 ggc ggc ggc agc ggt ggc ggc ggc gcc ccc cgg cgg gag ccg gtc cct    384
118 Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro
119         115                 120                 125
120 ttc ccg tcg ggg agc gcg ggg ccg ggg ccc agg gga ccc cgg gcc acg    432
121 Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr
122     130                 135                 140
123 gag agc ggg aag agg atg gat tgc ccg gcc ctc ccc ccc gga tgg aag    480
124 Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys
125 145                 150                 155                 160
126 aag gag gaa gtg atc cga aaa tct ggg cta agt gct ggc aag agc gat    528
127 Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp
128             165                 170                 175
129 gtc tac tac ttc agt cca agt ggt aag aag ttc aga agc aag cct cag    576
130 Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
131             180                 185                 190
132 ttg gca agg tac ctg gga aat act gtt gat ctc agc agt ttt gac ttc    624
133 Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe
134         195                 200                 205
135 aga act gga aag atg atg cct agt aaa tta cag aag aac aaa cag aga    672
136 Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg
137     210                 215                 220
138 ctg cga aac gat cct ctc aat caa aat aag ggt aaa cca gac ttg aat    720
139 Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn
140 225                 230                 235                 240
141 aca aca ttg cca att aga caa aca gca tca att ttc aaa caa ccg gta    768
142 Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
143         245                 250                 255
144 acc aaa gtc aca aat cat cct agt aat aaa gtg aaa tca gac cca caa    816
145 Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
146         260                 265                 270
147 cga atg aat gaa cag cca cgt cag ctt ttc tgg gag aag agg cta caa    864
148 Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln
149         275                 280                 285
150 gga ctt agt gca tca gat gta aca gaa caa att ata aaa acc atg gaa    912
151 Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu
152     290                 295                 300
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Input Set : **A:\766.43 Sequence Listing.txt**
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153 cta ccc aaa ggt ctt caa gga gtt ggt cca ggt agc aat gat gag acc   960
154 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr
155 305             310             315             320
156 ctt tta tct gct gtt gcc agt gct ttg cac aca agc tct gcg cca atc  1008
157 Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile
158             325             330             335
159 aca ggg caa gtc tcc gct gct gtg gaa aag aac cct gct gtt tgg ctt  1056
160 Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu
161             340             345             350
162 aac aca tct caa ccc ctc tgc aaa gct ttt att gtc aca gat gaa gac  1104
163 Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp
164             355             360             365
165 atc agg aaa cag gaa gag cga gta cag caa gta cgc aag aaa ttg gaa  1152
166 Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu
167     370             375             380
168 gaa gca ctg atg gca gac atc ttg tcg cga gct gct gat aca gaa gag  1200
169 Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu
170 385             390             395             400
171 atg gat att gaa atg gac agt gga gat gaa gcc                       1233
172 Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala
173             405             410
174 <210> SEQ ID NO: 3
175 <211> LENGTH: 196
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
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W--> 178 **<400> SEQUENCE: 3**

```
179 Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala
180 1           5               10              15
181 His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg
182             20              25              30
183 Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu
184         35              40              45
185 Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg
186     50              55              60
187 Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu
188 65              70              75              80
189 Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys
190             85              90              95
191 Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro
192             100             105             110
193 Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg
194         115             120             125
195 Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg
196     130             135             140
197 Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys
198 145             150             155             160
199 Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu
200             165             170             175
201 Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp
```

```
202              180                185                190
203 Thr Asp Val Arg
204          195
205 <210> SEQ ID NO: 4
206 <211> LENGTH: 588
207 <212> TYPE: DNA
208 <213> ORGANISM: Homo sapiens
209 <220> FEATURE:
210 <221> NAME/KEY: CDS
211 <223> OTHER INFORMATION: (1)..(591)
212 <400> SEQUENCE: 4
213 atg agg acc ttg gct tgc ctg ctg ctc ctc ggc tgc gga tac ctc gcc     48
214 Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala
215  1               5                  10                  15
216 cat gtt ctg gcc gag gaa gcc gag atc ccc cgc gag gtg atc gag agg     96
217 His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg
218          20                  25                  30
219 ctg gcc cgc agt cag atc cac agc atc cgg gac ctc cag cga ctc ctg    144
220 Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu
221          35                  40                  45
222 gag ata gac tcc gta ggg agt gag gat tct ttg gac acc agc ctg aga    192
223 Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg
224     50                  55                  60
225 gct cac ggg gtc cac gcc act aag cat gtg ccc gag aag cgg ccc ctg    240
226 Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu
227  65                  70                  75                  80
228 ccc att cgg agg aag aga agc atc gag gaa gct gtc ccc gct gtc tgc    288
229 Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys
230               85                  90                  95
231 aag acc agg acg gtc att tac gag att cct cgg agt cag gtc gac ccc    336
232 Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro
233          100                 105                 110
234 acg tcc gcc aac ttc ctg atc tgg ccc ccg tgc gtg gag gtg aaa cgc    384
235 Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg
236          115                 120                 125
237 tgc acc ggc tgc tgc aac acg agc agt gtc aag tgc cag ccc tcc cgc    432
238 Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg
239     130                 135                 140
240 gtc cac cac cgc agc gtc aag gtg gcc aag gtg gaa tac gtc agg aag    480
241 Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys
242 145                 150                 155                 160
243 aag cca aaa tta aaa gaa gtc cag gtg agg tta gag gag cat ttg gag    528
244 Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu
245                 165                 170                 175
246 tgc gcc tgc gcg acc aca agc ctg aat ccg gat tat cgg gaa gag gac    576
247 Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp
248          180                 185                 190
249 acg gat gtg agg                                                    588
250 Thr Asp Val Arg
```

VERIFICATION SUMMARY   DATE: 04/04/2002
PATENT APPLICATION: **US/09/749,728B**   TIME: 14:00:08

Input Set : **A:\766.43 Sequence Listing.txt**
Output Set: **N:\CRF3\04042002\I749728B.raw**

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L:35   M:283 W: Missing Blank Line separator, <400> field identifier
L:92   M:283 W: Missing Blank Line separator, <220> field identifier
L:95   M:283 W: Missing Blank Line separator, <400> field identifier
L:178  M:283 W: Missing Blank Line separator, <400> field identifier
L:209  M:283 W: Missing Blank Line separator, <220> field identifier
L:212  M:283 W: Missing Blank Line separator, <400> field identifier
L:256  M:283 W: Missing Blank Line separator, <400> field identifier
L:292  M:283 W: Missing Blank Line separator, <220> field identifier
L:295  M:283 W: Missing Blank Line separator, <400> field identifier
L:347  M:283 W: Missing Blank Line separator, <400> field identifier
L:372  M:283 W: Missing Blank Line separator, <220> field identifier
L:375  M:283 W: Missing Blank Line separator, <400> field identifier
L:410  M:283 W: Missing Blank Line separator, <400> field identifier
L:457  M:283 W: Missing Blank Line separator, <220> field identifier
L:460  M:283 W: Missing Blank Line separator, <400> field identifier
L:528  M:283 W: Missing Blank Line separator, <400> field identifier
L:589  M:283 W: Missing Blank Line separator, <220> field identifier
L:592  M:283 W: Missing Blank Line separator, <400> field identifier
L:681  M:283 W: Missing Blank Line separator, <400> field identifier
L:750  M:283 W: Missing Blank Line separator, <220> field identifier
L:753  M:283 W: Missing Blank Line separator, <400> field identifier
L:854  M:283 W: Missing Blank Line separator, <400> field identifier
L:905  M:283 W: Missing Blank Line separator, <220> field identifier
L:908  M:283 W: Missing Blank Line separator, <400> field identifier
L:982  M:283 W: Missing Blank Line separator, <400> field identifier
L:1046 M:283 W: Missing Blank Line separator, <220> field identifier
L:1049 M:283 W: Missing Blank Line separator, <400> field identifier
L:1144 M:283 W: Missing Blank Line separator, <400> field identifier
L:1215 M:283 W: Missing Blank Line separator, <220> field identifier
L:1218 M:283 W: Missing Blank Line separator, <400> field identifier
L:1322 M:283 W: Missing Blank Line separator, <400> field identifier
L:1355 M:283 W: Missing Blank Line separator, <220> field identifier
L:1358 M:283 W: Missing Blank Line separator, <400> field identifier
L:1405 M:283 W: Missing Blank Line separator, <400> field identifier
L:1438 M:283 W: Missing Blank Line separator, <220> field identifier
L:1441 M:283 W: Missing Blank Line separator, <400> field identifier
L:1488 M:283 W: Missing Blank Line separator, <400> field identifier
L:1545 M:283 W: Missing Blank Line separator, <220> field identifier
L:1548 M:283 W: Missing Blank Line separator, <400> field identifier
L:1631 M:283 W: Missing Blank Line separator, <400> field identifier
L:1690 M:283 W: Missing Blank Line separator, <220> field identifier
L:1693 M:283 W: Missing Blank Line separator, <400> field identifier
L:1779 M:283 W: Missing Blank Line separator, <400> field identifier
L:1839 M:283 W: Missing Blank Line separator, <220> field identifier
L:1842 M:283 W: Missing Blank Line separator, <400> field identifier
L:1931 M:283 W: Missing Blank Line separator, <400> field identifier
L:2078 M:283 W: Missing Blank Line separator, <220> field identifier
L:2081 M:283 W: Missing Blank Line separator, <400> field identifier
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VERIFICATION SUMMARY   DATE: 04/04/2002
PATENT APPLICATION: **US/09/749,728B**   TIME: 14:00:08

Input Set : **A:\766.43 Sequence Listing.txt**
Output Set: **N:\CRF3\04042002\I749728B.raw**

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L:2270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32
L:2273 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32
L:2276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32
L:2279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32
L:2282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32
L:2285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32
L:2288 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32
L:2291 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32
L:2299 M:283 W: Missing Blank Line separator, <220> field identifier
L:2301 M:283 W: Missing Blank Line separator, <400> field identifier
L:3142 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:71
L:3153 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:72
L:3164 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:73
L:3175 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:74
L:3186 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:75
L:3197 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:76
L:3208 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:77
L:3219 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:78
L:3230 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:79
L:3241 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:80
```